

SEQUENCE LISTING

<110> Glucksmann, Maria A.
Kadambi, Vivek

<120> 33358, A NOVEL HUMAN ANKYRIN FAMILY MEMBER AND USES THEREOF

<130> MNI-162CP

<150> 60/212,222

<151> 2000-06-16

<160> 3

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1538

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (75)...(1046)

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                Met Glu Asp Gly Pro Val Phe Tyr Gly Phe Lys Asn
                  1                5                10

att ttt att aca atg ttt gct acg ttt ttt ttc ttt aag ctt tta att 158
Ile Phe Ile Thr Met Phe Ala Thr Phe Phe Phe Phe Lys Leu Leu Ile
      15                20                25

aaa gtt ttt ttg gct ctc cta acc cat ttc tat atc gtc aaa gga aat 206
Lys Val Phe Leu Ala Leu Leu Thr His Phe Tyr Ile Val Lys Gly Asn
      30                35                40

aga aaa gaa gcg gct agg ata gca gaa gag atc tat ggt gga att tca 254
Arg Lys Glu Ala Ala Arg Ile Ala Glu Glu Ile Tyr Gly Gly Ile Ser
      45                50                55                60

gat tgc tgg gct gat cga tcc cca ctt cat gaa gct gca gct cag ggg 302
Asp Cys Trp Ala Asp Arg Ser Pro Leu His Glu Ala Ala Ala Gln Gly
      65                70                75

cgc tta ctg gcc ctt aaa act tta att gca caa ggt gtc aat gtg aac 350
Arg Leu Leu Ala Leu Lys Thr Leu Ile Ala Gln Gly Val Asn Val Asn
      80                85                90

ctt gtg aca att aac cgg gtg tct tct ctc cac gag gca tgc ctt gga 398
Leu Val Thr Ile Asn Arg Val Ser Ser Leu His Glu Ala Cys Leu Gly
      95                100                105
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09884870-061801

ggt cac gtg gcc tgt gcc aaa gcc tta ttg gaa aat ggt gca cac gtc 446
 Gly His Val Ala Cys Ala Lys Ala Leu Leu Glu Asn Gly Ala His Val
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aat gga gtg aca gtt cac gga gcc aca ccc ctc ttc aat gct tgc tgc 494
 Asn Gly Val Thr Val His Gly Ala Thr Pro Leu Phe Asn Ala Cys Cys
 125 130 135 140

agc ggc agt gct gca tgt gtc aat gtg ctg ctg gag ttc gga gcc aag 542
 Ser Gly Ser Ala Ala Cys Val Asn Val Leu Leu Glu Phe Gly Ala Lys
 145 150 155

gcc cag ttg gag gtg cac ctg gcc tcg ccc atc cat gag gca gtg aag 590
 Ala Gln Leu Glu Val His Leu Ala Ser Pro Ile His Glu Ala Val Lys
 160 165 170

aga ggt cac aga gag tgc atg gag atc ctg ctg gca aat aat gtt aac 638
 Arg Gly His Arg Glu Cys Met Glu Ile Leu Leu Ala Asn Asn Val Asn
 175 180 185

att gac cat gag gtg cct cag ctc gga act ccc cta tat gtg gcc tgc 686
 Ile Asp His Glu Val Pro Gln Leu Gly Thr Pro Leu Tyr Val Ala Cys
 190 195 200

acc tac cag agg gta gac tgt gtg aag aaa ctt cta gaa tta gga gcc 734
 Thr Tyr Gln Arg Val Asp Cys Val Lys Lys Leu Leu Glu Leu Gly Ala
 205 210 215 220

agt gtc gac cat ggc cag tgg ctg gac acc cca ctc cat gct gca gcg 782
 Ser Val Asp His Gly Gln Trp Leu Asp Thr Pro Leu His Ala Ala Ala
 225 230 235

agg cag tcc aat gtg gag gtc atc cac ctg cta acc gac tat gga gct 830
 Arg Gln Ser Asn Val Glu Val Ile His Leu Leu Thr Asp Tyr Gly Ala
 240 245 250

aac ctg aag cgt aga aat gct cag ggc aaa agt gcg ctt gat ctg gcg 878
 Asn Leu Lys Arg Arg Asn Ala Gln Gly Lys Ser Ala Leu Asp Leu Ala
 255 260 265

gct cca aaa agc agc gtg gag cag gca ctc ttg ctc cgt gaa ggc cca 926
 Ala Pro Lys Ser Ser Val Glu Gln Ala Leu Leu Leu Arg Glu Gly Pro
 270 275 280

cct gct ctt tcc cag ctc tgc cgc ctg tgt gtc cgg aag tgt ctc ggt 974
 Pro Ala Leu Ser Gln Leu Cys Arg Leu Cys Val Arg Lys Cys Leu Gly
 285 290 295 300

cga gca tgt cat caa gcc atc cac aag cta cat ctg cca gag cca ctc 1022
 Arg Ala Cys His Gln Ala Ile His Lys Leu His Leu Pro Glu Pro Leu
 305 310 315

gaa cga ttc ctc cta tac caa tag tcctaagtgt tcctgggaag atacttgga 1076
 Glu Arg Phe Leu Leu Tyr Gln *
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ttagctttta gctctttgtt gttaagaaac ttaaaagaac tgtgaagtag agtgaaaaca 1316
ataggctgtt ttttgatgat tcgggatctt cttgtacctt aaagtcaaca ttctgaatat 1376
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<210> 2
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Ala Leu Leu Thr His Phe Tyr Ile Val Lys Gly Asn Arg Lys Glu Ala
 35          40          45
Ala Arg Ile Ala Glu Glu Ile Tyr Gly Gly Ile Ser Asp Cys Trp Ala
 50          55          60
Asp Arg Ser Pro Leu His Glu Ala Ala Ala Gln Gly Arg Leu Leu Ala
 65          70          75          80
Leu Lys Thr Leu Ile Ala Gln Gly Val Asn Val Asn Leu Val Thr Ile
 85          90          95
Asn Arg Val Ser Leu His Glu Ala Cys Leu Gly Gly His Val Ala
100          105          110
Cys Ala Lys Ala Leu Leu Glu Asn Gly Ala His Val Asn Gly Val Thr
115          120          125
Val His Gly Ala Thr Pro Leu Phe Asn Ala Cys Cys Ser Gly Ser Ala
130          135          140
Ala Cys Val Asn Val Leu Leu Glu Phe Gly Ala Lys Ala Gln Leu Glu
145          150          155          160
Val His Leu Ala Ser Pro Ile His Glu Ala Val Lys Arg Gly His Arg
165          170          175
Glu Cys Met Glu Ile Leu Leu Ala Asn Asn Val Asn Ile Asp His Glu
180          185          190
Val Pro Gln Leu Gly Thr Pro Leu Tyr Val Ala Cys Thr Tyr Gln Arg
195          200          205
Val Asp Cys Val Lys Lys Leu Leu Glu Leu Gly Ala Ser Val Asp His
210          215          220
Gly Gln Trp Leu Asp Thr Pro Leu His Ala Ala Arg Gln Ser Asn
225          230          235          240
Val Glu Val Ile His Leu Leu Thr Asp Tyr Gly Ala Asn Leu Lys Arg
245          250          255
Arg Asn Ala Gln Gly Lys Ser Ala Leu Asp Leu Ala Ala Pro Lys Ser
260          265          270
Ser Val Glu Gln Ala Leu Leu Leu Arg Glu Gly Pro Pro Ala Leu Ser
275          280          285
Gln Leu Cys Arg Leu Cys Val Arg Lys Cys Leu Gly Arg Ala Cys His
290          295          300
Gln Ala Ile His Lys Leu His Leu Pro Glu Pro Leu Glu Arg Phe Leu
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Leu Tyr Gln

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09884870.061.601

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 <212> DNA
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<220>
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atg ttt gct acg ttt ttt ttc ttt aag ctt tta att aaa gtt ttt ttg 96
 Met Phe Ala Thr Phe Phe Phe Phe Lys Leu Leu Ile Lys Val Phe Leu
 20 25 30

gct ctc cta acc cat ttc tat atc gtc aaa gga aat aga aaa gaa gcg 144
 Ala Leu Leu Thr His Phe Tyr Ile Val Lys Gly Asn Arg Lys Glu Ala
 35 40 45

gct agg ata gca gaa gag atc tat ggt gga att tca gat tgc tgg gct 192
 Ala Arg Ile Ala Glu Glu Ile Tyr Gly Gly Ile Ser Asp Cys Trp Ala
 50 55 60

gat cga tcc cca ctt cat gaa gct gca gct cag ggg cgc tta ctg gcc 240
 Asp Arg Ser Pro Leu His Glu Ala Ala Ala Gln Gly Arg Leu Leu Ala
 65 70 75 80

ctt aaa act tta att gca caa ggt gtc aat gtg aac ctt gtg aca att 288
 Leu Lys Thr Leu Ile Ala Gln Gly Val Asn Val Asn Leu Val Thr Ile
 85 90 95

aac cgg gtg tct tct ctc cac gag gca tgc ctt gga ggt cac gtg gcc 336
 Asn Arg Val Ser Ser Leu His Glu Ala Cys Leu Gly Gly His Val Ala
 100 105 110

tgt gcc aaa gcc tta ttg gaa aat ggt gca cac gtc aat gga gtg aca 384
 Cys Ala Lys Ala Leu Leu Glu Asn Gly Ala His Val Asn Gly Val Thr
 115 120 125

gtt cac gga gcc aca ccc ctc ttc aat gct tgc tgc agc ggc agt gct 432
 Val His Gly Ala Thr Pro Leu Phe Asn Ala Cys Cys Ser Gly Ser Ala
 130 135 140

gca tgt gtc aat gtg ctg ctg gag ttc gga gcc aag gcc cag ttg gag 480
 Ala Cys Val Asn Val Leu Leu Glu Phe Gly Ala Lys Ala Gln Leu Glu
 145 150 155 160

gtg cac ctg gcc tcg ccc atc cat gag gca gtg aag aga ggt cac aga 528
 Val His Leu Ala Ser Pro Ile His Glu Ala Val Lys Arg Gly His Arg
 165 170 175

gag tgc atg gag atc ctg ctg gca aat aat gtt aac att gac cat gag 576
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09084970.061604

180	185	190	
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Val Pro Gln Leu Gly Thr Pro Leu Tyr Val Ala Cys Thr Tyr Gln Arg			
195	200	205	
gta gac tgt gtg aag aaa ctt cta gaa tta gga gcc agt gtc gac cat			672
Val Asp Cys Val Lys Lys Leu Leu Glu Leu Gly Ala Ser Val Asp His			
210	215	220	
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Gly Gln Trp Leu Asp Thr Pro Leu His Ala Ala Ala Arg Gln Ser Asn			
225	230	235	240
gtg gag gtc atc cac ctg cta acc gac tat gga gct aac ctg aag cgt			768
Val Glu Val Ile His Leu Leu Thr Asp Tyr Gly Ala Asn Leu Lys Arg			
245	250	255	
aga aat gct cag ggc aaa agt gcg ctt gat ctg gcg gct cca aaa agc			816
Arg Asn Ala Gln Gly Lys Ser Ala Leu Asp Leu Ala Ala Pro Lys Ser			
260	265	270	
agc gtg gag cag gca ctc ttg ctc cgt gaa ggc cca cct gct ctt tcc			864
Ser Val Glu Gln Ala Leu Leu Leu Arg Glu Gly Pro Pro Ala Leu Ser			
275	280	285	
cag ctc tgc cgc ctg tgt gtc cgg aag tgt ctc ggt cga gca tgt cat			912
Gln Leu Cys Arg Leu Cys Val Arg Lys Cys Leu Gly Arg Ala Cys His			
290	295	300	
caa gcc atc cac aag cta cat ctg cca gag cca ctc gaa cga ttc ctc			960
Gln Ala Ile His Lys Leu His Leu Pro Glu Pro Leu Glu Arg Phe Leu			
305	310	315	320
cta tac caa tag			972
Leu Tyr Gln *			

09884870-061301